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N-TERMINAL AMINO ACID SEQUENCE OF EXFOLIATIVE TOXINS FROM TWO S--ETC(U)
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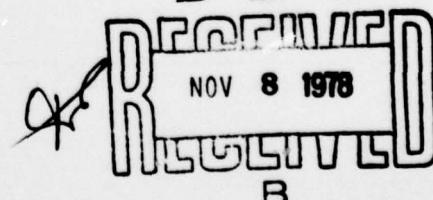
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ABSTRACT

N-terminal amino acid sequences of the exfoliative toxins from two strains of Staphylococcus aureus exhibited no obvious homology. However, a single unit alignment shift revealed significant similarities.

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An exfoliative toxin from Staphylococcus aureus has been implicated as the cause of scalded-skin syndrome (5). In 1975 we reported the isolation and purification of one form of this toxin from S. aureus strain TA (3). In an accompanying article in this Journal (4) we have described the isolation from strain DI of a second form of exfoliatin. Although the two toxins have identical specific activities and differ only slightly in molecular weights and amino acid compositions, they show no serologic cross-reaction. As part of their characterization, we report here the primary structure of the amino-terminal portions of these toxins.

Intact protein from S. aureus strains TA and DI was subjected to automated degradation on a Beckman 890 C sequencer. The Beckman standard fast Quadrol protein program proved superior to the dimethylallylamine peptide program in determining the amino acid sequence for both proteins. Amino acid residues were identified directly from the phenylthiohydantoin (PTH) derivatives. Gas chromatography (1), the ascending chromatographic method of Jeppsson and Sjöquist (2) and the gradient elution system of Tarr (6) were used. Acid hydrolysis of the PTH derivatives, followed by identification on a Beckman 121-MB amino acid analyzer of the products, was the final method of residue identification (6).

The amino acid sequence was obtained for the first 26 and 23 residues of the toxins from strains DI and TA, respectively. Both these sequences are given below.

<u>Strain</u>	1	2	3	4	5	6	7	8	9	10	11	12	13
DI	Lys	Glu	Tyr	Ala	Ala	Glu	Glu	Ile	Arg	Lys	Leu	Lys	Glu
TA	Glu	Val	Thr	Ala	Glu	Glu	Ile	Lys	Lys	His	Glu	Glu	Lys
	14	15	16	17	18	19	20	21	22	23	24	25	26
DI	Lys	Phe	Glu	Val	Pro	Pro	Thr	Asp	Lys	Glu	Leu	Tyr	Thr
TA	Trp	Asp	Lys	Tyr	Tyr	Gly	Val	X	Asx	Phe			

A direct comparison of these sequences shows little obvious homology. However, if the amino-terminal residue of the TA protein is compared with the second residue of the DI protein, and so on, substantial homology is observed. The results of this alignment are shown below.

<u>Strain</u>	1	2	3	4	5	6	7	8	9	10	11	12	13	14
DI	Lys	Glu	Tyr	Ala	Ala	Glu	Glu	Ile	Arg	Lys	Leu	Lys	Glu	Lys
TA		Glu	Val	Thr	Ala	Glu	Glu	Ile	Lys	Lys	His	Glu	Glu	Lys

Eight of the first 13 residues of the toxin from TA are now identical to those in the DI toxin. These are enclosed in boxes. Four additional residues at position 4, 9, 11 and 12 are underlined. Single base changes in the codons for these amino acids can account for the differences. The identical specific activity of the two molecular species of toxin suggests that additional segments possessing significant homology exist. Indeed one would anticipate that the molecules have

similar secondary and tertiary folding. The toxin from strain TA has been crystallized and preliminary X-ray diffraction patterns obtained (7). Establishment of its three-dimensional structure will be of great value in elucidation of the mechanism of exfoliation.

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